

S3 Table. Percentage of template-switching reads.

Enzyme	Double	Single (fwd)	Single (rev)	Total reads
<i>lacZ inversion region 1843..1981</i>				
Taq	n.d.	n.d. ^a	n.d.	29,047
Q5	n.d.	n.d. ^a	0.003%	104,812
Phusion	n.d.	n.d. ^a	n.d.	73,085
Deep Vent	0.184%	0.006% ^a	1.350%	67,473
Pfu	n.d.	0.001% ^a	0.421%	67,656
PrimeSTAR GXL	n.d.	n.d. ^a	n.d.	73,847
KOD	0.011%	n.d. ^a	n.d.	55,712
Kapa HiFi HotStart ReadyMix	n.d.	n.d. ^a	0.006%	36,229
Deep Vent (exo-)	n.d.	n.d. ^a	0.028%	31,644
<i>lacZ inversion region 3083..3103</i>				
Taq	n.d.	n.d.	n.d. ^b	31,566
Q5	0.001%	n.d.	n.d. ^b	104,340
Phusion	0.024%	n.d.	n.d. ^b	71,609
Deep Vent	0.163%	0.004%	n.d. ^b	66,684
Pfu	0.003%	n.d.	n.d. ^b	67,492
PrimeSTAR GXL	0.004%	n.d.	n.d. ^b	73,653
KOD	0.400%	0.002%	n.d. ^b	55,464
Kapa HiFi HotStart ReadyMix	0.003%	n.d.	n.d. ^b	36,185
Deep Vent (exo-)	0.010%	n.d.	n.d. ^b	40,651

^a The expected length of template switching read is 227 nt, which is not expected to be detected because its size is below the threshold for sequencing by MagBead loading on the PacBio RSII.

^b The expected length of template switching read is 117 nt, which is not expected to be detected because its size is below the threshold for sequencing by MagBead loading on the PacBio RSII.